EAST Search History

Ref #	Hits	Search Query	DBs	Default Operator	Plurals	Time Stamp
L1	4	krix1 or (krix adj "1") or (lmbp adj 5089CB) or (lmbp5089cb)	USPAT; EPO; JPO; DERWENT	ADJ	ON	2006/09/05 12:44
L2	6	krix1 or (krix adj "1") or (lmbp adj 5089CB) or (lmbp5089cb)	US-PGPUB; USPAT; EPO; JPO; DERWENT	ADJ	ON	2006/09/05 12:44
L3	10886	fviii or fviiia or (factor adj (viii or viiia or eight)) or factor-viii or factor-viiia	US-PGPUB; USPAT; EPO; JPO; DERWENT	ADJ	ON	2006/09/05 12:45
L4	257464	antibody or antibodies or immunoglobulin or immunoglobulins or immunoadhesin	US-PGPUB; USPAT; EPO; JPO; DERWENT	ADJ	ON	2006/09/05 12:45
L5	35511	sirs or sepsis or (systemic adj inflammatory adj response adj syndrome) or dic	US-PGPUB; USPAT; EPO; JPO; DERWENT	ADJ	ON	2006/09/05 12:45
L6	581945	c1	US-PGPUB; USPAT; EPO; JPO; DERWENT	ADJ	ON	2006/09/05 12:45
L7	259	(L3 same L4) and L5	US-PGPUB; USPAT; EPO; JPO; DERWENT	ADJ	ON	2006/09/05 12:45
L8	22	L7 and L6	USPAT; EPO; JPO; DERWENT	ADJ	ON	2006/09/05 12:46
L9	62	L7 and L6	US-PGPUB; USPAT; EPO; JPO; DERWENT	ADJ	ON	2006/09/05 12:46
L10	216	jacquemin.in.	US-PGPUB; USPAT; EPO; JPO; DERWENT	ADJ	ON	2006/09/05 12:46
L11	40	(saint-remy.in.) or (saintremy.in.) or ((saint adj remy).in.)	US-PGPUB; USPAT; EPO; JPO; DERWENT	ADJ	ON	2006/09/05 12:47
L12	34	(l10 or l11) and l4	US-PGPUB; USPAT; EPO; JPO; DERWENT	ADJ	ON	2006/09/05 12:48

SCORE Search Results Details for Application 10044569 and Search Result us-10-044-569b-6.rag.

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start

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OM protein - protein search, using sw model

Run on:          August  9, 2006, 01:42:08 ; Search time 115.35 Seconds
                                             (without alignments)
                                             618.341 Million cell updates/sec

Title:           US-10-044-569B-6
Perfect score:   837
Sequence:        1 MDWTWRILFLVAAATGAHSQ..........GYTSHYFDYWGRGTLVTVSS 156

Scoring table:   BLOSUM62
                 Gapop 10.0 , Gapext 0.5

Searched:        2589679 seqs, 457216429 residues

Total number of hits satisfying chosen parameters:       2589679

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

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    Pred. No. is the number of results predicted by chance to have a
    score greater than or equal to the score of the result being printed,
    and is derived by analysis of the total score distribution.

                            SUMMARIES
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Result No.	Score	% Query Match	Length	DB	ID	Description
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3	837	100.0	165	9	ADY34082	Ady34082 Factor VI
4	735	87.8	288	9	ADY34106	Ady34106 Factor VI
5	611.5	73.1	471	7	ADE28427	Ade28427 Human ant
6	607	72.5	470	5	AAU74296	Aau74296 Anti-huma
7	602	71.9	141	9	ADY16604	Ady16604 PRO polyp
8	599.5	71.6	576	8	ADF69325	Adf69325 Human lun
9	587.5	70.2	139	9	ADX98261	Adx98261 Human ant
10	586	70.0	146	2	AAW22841	Aaw22841 Human ant
11	574.5	68.6	139	9	ADX98257	Adx98257 Human ant
12	550.5	65.8	236	4	AAB36215	Aab36215 Human imm
13	550	65.7	117	2	AAR66296	Aar66296 Human imm
14	547.5	65.4	148	3	AAY96295	Aay96295 Human IGF
15	547.5	65.4	198	8	ADF69324	Adf69324 Human lun
16	544.5	65.1	145	6	ABP57367	Abp57367 Anti-TRAI
17	540.5	64.6	146	3	AAB53510	Aab53510 Human col
18	540	64.5	476	2	AAW88464	Aaw88464 Monoclona
19	539	64.4	250	5	ABP45711	Abp45711 Human BLy
20	539	64.4	250	7	ADG96538	Adg96538 Single ch
21	539	64.4	250	9	AED78591	Aed78591 Human B L
22	537	64.2	134	9	ADZ57712	Adz57712 Germline
23	536	64.0	136	9	ADZ57729	Adz57729 Anti-cMet
24	532	63.6	136	9	ADZ57728	Adz57728 Anti-cMet
25	532	63.6	149	2	AAY24370	Aay24370 Human mon
26	532	63.6	172	8	ADK52436	Adk52436 Human ant
27	531	63.4	136	9	ADZ57732	Adz57732 Anti-cMet
28	530	63.3	464	9	AEA41032	Aea41032 Human ant
29	529.5	63.3	746	4	AAU31804	Aau31804 Novel hum
30	528.5	63.1	135	3	AAY80290	Aay80290 Humanised
31	528.5	63.1	281	8	ADP03813	Adp03813 Human ant
32	528.5	63.1	286	8	ADP03811	Adp03811 Human ant
33	528	63.1	136	9	ADZ57727	Adz57727 Anti-cMet
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38	527	63.0	250	9	AED78592	Aed78592 Human B L
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44	523.5	62.5	139	2	AAW62204	Aaw62204 Humanised
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ALIGNMENTS

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AAB47059
ID   AAB47059 standard; protein; 156 AA.
XX
AC   AAB47059;
XX
DT   08-MAY-2001 (first entry)

SCORE Search Results Details for Application 10044569 and Search Result us-10-044-569b-6.rai.

This page gives you Search Results detail for the Application 10044569 and Search Result us-10-044-569b-6.rai.

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                          GenCore version 5.1.9
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OM protein - protein search, using sw model

Run on:          August  9, 2006, 01:59:49 ; Search time 30.3553 Seconds
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Title:           US-10-044-569B-6
Perfect score:   837
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Scoring table:   BLOSUM62
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Searched:        650591 seqs, 87530628 residues

Total number of hits satisfying chosen parameters:       650591

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
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     Pred. No. is the number of results predicted by chance to have a
     score greater than or equal to the score of the result being printed,
     and is derived by analysis of the total score distribution.

                              SUMMARIES
                       %
Result                Query
   No.    Score  Match Length DB  ID                        Description
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     2   550.5    65.8    236   2   US-09-049-672A-13       Sequence 13, Appl
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     5     532    63.6    149   2   US-09-582-337-8         Sequence 8, Appli
     6   525.5    62.8    146   2   US-09-582-337-12        Sequence 12, Appl
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     8   523.5    62.5    139   2   US-09-269-921-123       Sequence 123, App
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    12   519.5    62.1    139   2   US-09-269-921-108       Sequence 108, App
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    14   518.5    61.9    139   2   US-09-269-921-124       Sequence 124, App
    15   517.5    61.8    137   2   US-08-513-968-38        Sequence 38, Appl
    16   517.5    61.8    139   2   US-09-355-925-7         Sequence 7, Appli
    17   517.5    61.8    139   2   US-09-269-921-121       Sequence 121, App
    18   517.5    61.8    139   2   US-09-269-921-125       Sequence 125, App
    19   516.5    61.7    139   2   US-09-269-921-109       Sequence 109, App
    20   516.5    61.7    139   2   US-09-269-921-118       Sequence 118, App
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    33   513.5    61.4    139   2   US-09-355-925-8         Sequence 8, Appli
    34   513.5    61.4    139   2   US-09-269-921-110       Sequence 110, App
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    36   512.5    61.2    135   1   US-08-137-117D-100      Sequence 100, App
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    41   510.5    61.0    139   2   US-09-269-921-120       Sequence 120, App
    42     509    60.8    142   1   US-08-561-521-17        Sequence 17, Appl
    43     509    60.8    142   5   PCT-US95-01219-17       Sequence 17, Appl
    44     508    60.7    470   2   US-09-499-662-157       Sequence 157, App
    45   506.5    60.5    467   1   US-07-916-098A-45       Sequence 45, Appl
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ALIGNMENTS

RESULT 1
US-09-859-053-28
; Sequence 28, Application US/09859053
; Patent No. 6803039
; GENERAL INFORMATION:
; APPLICANT: Tsuji, Takashi
; APPLICANT: Tezuka, Katsunari
; APPLICANT: Hori, No. 6803039uaki
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODY AGAINST A
; TITLE OF INVENTION: COSTIMULATORY SIGNAL TRANSDUCTION MOLECULE AILIM AND

SCORE Search Results Details for Application 10044569 and Search Result us-10-044-569b-6.rapbm.

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OM protein - protein search, using sw model

Run on:          August  9, 2006, 02:25:55 ; Search time 99.5127 Seconds
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Title:           US-10-044-569B-6
Perfect score:   837
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Scoring table:   BLOSUM62
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Total number of hits satisfying chosen parameters:      2097797

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
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           4:    /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10A_PUBCOMB.pep:*
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     Pred. No. is the number of results predicted by chance to have a
     score greater than or equal to the score of the result being printed,
     and is derived by analysis of the total score distribution.

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Result               Query
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4	607	72.5	470	4	US-10-800-250-28	Sequence 28, Appl
5	607	72.5	470	4	US-10-625-105-28	Sequence 28, Appl
6	587.5	70.2	139	5	US-10-893-576-33	Sequence 33, Appl
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16	539	64.4	250	4	US-10-293-418-1722	Sequence 1722, Ap
17	539	64.4	250	6	US-11-054-515-1722	Sequence 1722, Ap
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39	522.5	62.4	614	4	US-10-389-223A-2	Sequence 2, Appli
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41	521.5	62.3	469	6	US-11-031-485-42	Sequence 42, Appl
42	521	62.2	462	5	US-10-910-901-2	Sequence 2, Appli
43	520.5	62.2	135	5	US-10-837-904-109	Sequence 109, App
44	520.5	62.2	197	4	US-10-264-049-4263	Sequence 4263, Ap
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ALIGNMENTS

RESULT 1
US-10-044-569B-6
; Sequence 6, Application US/10044569B
; Publication No. US20030175268A1
; GENERAL INFORMATION:
; APPLICANT: D. Collen Research Foundation vzw
; APPLICANT: Jacquemin, Marc G
; APPLICANT: Saint-Remy, Jean-Marie R
; TITLE OF INVENTION: Method and pharmaceutical composition for preventing
; TITLE OF INVENTION: and/or treating systemic inflammatory response syndrome
; FILE REFERENCE: C1968

SCORE Search Results Details for Application 10044569 and Search Result us-10-044-569b-6.rapbn.

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start

Go Back to previous

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OM protein - protein search, using sw model

Run on:          August  9, 2006, 02:27:00 ; Search time 15.3096 Seconds
                                             (without alignments)
                                             681.831 Million cell updates/sec

Title:           US-10-044-569B-6
Perfect score:   837
Sequence:        1 MDWTWRILFLVAAATGAHSQ..........GYTSHYFDYWGRGTLVTVSS 156

Scoring table:   BLOSUM62
                 Gapop 10.0 , Gapext 0.5

Searched:        236815 seqs, 66914042 residues

Total number of hits satisfying chosen parameters:     236815

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
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      Pred. No. is the number of results predicted by chance to have a
      score greater than or equal to the score of the result being printed,
      and is derived by analysis of the total score distribution.

                             SUMMARIES
                      %
Result             Query
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2	735	87.8	288	7	US-11-298-560-26	Sequence 26, Appl
3	611.5	73.1	471	7	US-11-211-917-46	Sequence 46, Appl
4	530	63.3	464	7	US-11-375-221-22	Sequence 22, Appl
5	517.5	61.8	139	6	US-10-533-104A-21	Sequence 21, Appl
6	514.5	61.5	122	7	US-11-211-917-110	Sequence 110, App
7	513.5	61.4	139	6	US-10-533-104A-22	Sequence 22, Appl
8	509	60.8	142	7	US-11-006-808-17	Sequence 17, Appl
9	507.5	60.6	126	7	US-11-211-917-42	Sequence 42, Appl
10	502	60.0	477	6	US-10-559-236-2	Sequence 2, Appli
11	493	58.9	150	7	US-11-298-560-46	Sequence 46, Appl
12	492.5	58.8	120	7	US-11-221-902-21	Sequence 21, Appl
13	492.5	58.8	447	7	US-11-221-902-10	Sequence 10, Appl
14	492.5	58.8	447	7	US-11-221-902-12	Sequence 12, Appl
15	490.5	58.6	477	7	US-11-293-697-4289	Sequence 4289, Ap
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17	483.5	57.8	120	7	US-11-304-986-22	Sequence 22, Appl
18	482.5	57.6	120	7	US-11-221-902-18	Sequence 18, Appl
19	482.5	57.6	447	7	US-11-221-902-8	Sequence 8, Appli
20	479.5	57.3	475	6	US-10-523-295-30	Sequence 30, Appl
21	479.5	57.3	475	6	US-10-523-295-32	Sequence 32, Appl
22	479	57.2	134	7	US-11-219-563-27	Sequence 27, Appl
23	479	57.2	464	7	US-11-219-563-132	Sequence 132, App
24	475.5	56.8	118	7	US-11-249-296-2	Sequence 2, Appli
25	475.5	56.8	118	7	US-11-249-296-72	Sequence 72, Appl
26	475.5	56.8	118	7	US-11-249-296-90	Sequence 90, Appl
27	473.5	56.6	120	7	US-11-221-902-19	Sequence 19, Appl
28	473.5	56.6	124	7	US-11-271-008-8	Sequence 8, Appli
29	473.5	56.6	447	7	US-11-221-902-84	Sequence 84, Appl
30	473.5	56.6	473	7	US-11-293-697-4284	Sequence 4284, Ap
31	471	56.3	126	7	US-11-094-132-71	Sequence 71, Appl
32	470	56.2	495	7	US-11-293-697-4277	Sequence 4277, Ap
33	466	55.7	119	7	US-11-291-140-27	Sequence 27, Appl
34	466	55.7	495	7	US-11-293-697-4085	Sequence 4085, Ap
35	463	55.3	476	7	US-11-293-697-4288	Sequence 4288, Ap
36	460.5	55.0	108	6	US-10-484-105-14	Sequence 14, Appl
37	460	55.0	129	7	US-11-006-808-45	Sequence 45, Appl
38	457	54.6	470	7	US-11-293-697-4292	Sequence 4292, Ap
39	456	54.5	143	7	US-11-224-664-26	Sequence 26, Appl
40	451	53.9	117	7	US-11-249-296-6	Sequence 6, Appli
41	451	53.9	124	6	US-10-981-300-49	Sequence 49, Appl
42	449	53.6	474	7	US-11-293-697-4282	Sequence 4282, Ap
43	447	53.4	118	7	US-11-375-221-111	Sequence 111, App
44	446.5	53.3	118	7	US-11-094-132-62	Sequence 62, Appl
45	446	53.3	98	7	US-11-221-902-52	Sequence 52, Appl

ALIGNMENTS

RESULT 1
US-11-298-560-2
; Sequence 2, Application US/11298560
; Publication No. US20060115474A1
; GENERAL INFORMATION:
; APPLICANT: Jacquemin, Marc
; APPLICANT: Saint-Remy, Jean-Marie
; TITLE OF INVENTION: Ligands For Use In Therapeutic Compositions For The Treatment o
; TITLE OF INVENTION: Hemostasis Disorders

SCORE Search Results Details for Application 100

This page gives you Search Results detail for the Application 10044569 and Search Result us-10-0₄
start

```
                           GenCore version 5.1.9
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OM protein - protein search, using sw model

Run on:         August  9, 2006, 01:50:34 ; Search time 18.7411 Seconds
                                             (without alignments)
                                             800.903 Million cell updates/sec

Title:          US-10-044-569B-6
Perfect score:  837
Sequence:       1 MDWTWRILFLVAAATGAHSQ..........GYTSHYFDYWGRGTLVTVSS 156

Scoring table:  BLOSUM62
                Gapop 10.0 , Gapext 0.5

Searched:       283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters:       283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :      PIR_80:*
                1:  pir1:*
                2:  pir2:*
                3:  pir3:*
                4:  pir4:*

          Pred. No. is the number of results predicted by chance to have a
          score greater than or equal to the score of the result being printed,
          and is derived by analysis of the total score distribution.
```

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	606.5	72.5	135	2	S49530	anti-Sm antibody V
2	591.5	70.7	171	2	S23623	Ig heavy chain V r
3	550	65.7	117	2	S18551	Ig heavy chain V r
4	549.5	65.7	136	2	S31600	Ig heavy chain V r
5	548	65.5	117	1	HVHU35	Ig heavy chain pre
6	540	64.5	117	2	S31680	Ig heavy chain V r
7	523.5	62.5	132	2	S31596	Ig heavy chain V r
8	521	62.2	160	2	PL0105	anti-PR2 erythrocy

9	517	61.8	148	2	S29257	Ig heavy chain V r
10	515	61.5	142	2	S19245	Ig heavy chain pre
11	505	60.3	129	2	S46393	Ig heavy chain V r
12	502	60.0	123	2	D33548	Ig heavy chain V-1
13	498	59.5	142	2	A32483	Ig heavy chain V r
14	493	58.9	117	2	S18553	Ig heavy chain V r
15	491	58.7	134	2	S21916	Ig heavy chain V r
16	490.5	58.6	118	2	S36265	Ig heavy chain V r
17	489	58.4	627	2	S14683	Ig mu chain precur
18	486	58.1	117	1	HVHUHG	Ig heavy chain pre
19	482.5	57.6	143	1	E1HUND	Ig heavy chain pre
20	477	57.0	117	2	S18552	Ig heavy chain V r
21	474	56.6	131	2	S21924	Ig heavy chain V r
22	465	55.6	117	2	PT0371	Ig gamma chain pre
23	464.5	55.5	139	1	MHMS18	Ig heavy chain pre
24	462.5	55.3	137	2	C41287	Ig heavy chain pre
25	460	55.0	117	2	S18554	Ig heavy chain V r
26	456	54.5	138	1	HVMST7	Ig heavy chain pre
27	454	54.2	104	2	S69899	Ig heavy chain V r
28	453.5	54.2	110	2	PH1669	Ig heavy chain V r
29	450.5	53.8	135	2	A30577	Ig heavy chain pre
30	450	53.8	138	2	E32513	Ig heavy chain pre
31	447	53.4	111	2	S21925	Ig heavy chain V r
32	446	53.3	98	2	S26938	Ig heavy chain V r
33	443	52.9	121	2	S20783	Ig heavy chain V r
34	439.5	52.5	137	1	G2MS43	Ig heavy chain pre
35	438.5	52.4	116	2	S31698	Ig heavy chain pre
36	438	52.3	98	2	S26912	Ig heavy chain V r
37	438	52.3	109	2	PH1668	Ig heavy chain V r
38	437.5	52.3	137	2	F29380	Ig heavy chain pre
39	437.5	52.3	474	1	G2MS11	Ig gamma-2b chain
40	436.5	52.2	116	2	S31667	Ig heavy chain V r
41	435.5	52.0	137	2	H32513	Ig heavy chain pre
42	435	52.0	127	2	S34014	Ig heavy chain V r
43	434	51.9	126	2	I44151	Ig heavy chain V r
44	433.5	51.8	137	2	E29380	Ig heavy chain pre
45	433.5	51.8	469	2	S37483	Ig gamma-2a chain

ALIGNMENTS

RESULT 1
S49530
anti-Sm antibody VH chain (VH1/DK1 or DM1/JH4b) - human
C;Species: Homo sapiens (man)
C;Date: 01-Feb-1995 #sequence_revision 12-May-1995 #text_change 23-Jul-1999
C;Accession: S49530
R;Mahmoudi, M.; Edwards, J.; Cairns, E.; Bell, D.
submitted to the EMBL Data Library, October 1994
A;Description: Molecular characterization of natural human anti-Sm autoantibodies.
A;Reference number: S48797.
A;Accession: S49530
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-135
A;Cross-references: UNIPARC:UPI00001166FF; EMBL:Z46348; NID:g560839; PIDN:CAA86467.1;
C;Superfamily: immunoglobulin V region; immunoglobulin homology
F;34-117/Domain: immunoglobulin homology

  Query Match   72.5%; Score 606.5; DB 2; Length 135;

SCORE Search Results Details for Application 10044569 and Search Result us-10-044-569b-6.rup.

This page gives you Search Results detail for the Application 10044569 and Search Result us-10-044-569b-6.rup.

start

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OM protein - protein search, using sw model

Run on:         August  9, 2006, 01:43:08 ; Search time 145.706 Seconds
                                            (without alignments)
                                            990.370 Million cell updates/sec

Title:          US-10-044-569B-6
Perfect score:  837
Sequence:       1 MDWTWRILFLVAAATGAHSQ..........GYTSHYFDYWGRGTLVTVSS 156

Scoring table:  BLOSUM62
                Gapop 10.0 , Gapext 0.5

Searched:       2849598 seqs, 925015592 residues

Total number of hits satisfying chosen parameters:      2849598

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :      UniProt_7.2:*
                1:  uniprot_sprot:*
                2:  uniprot_trembl:*

       Pred. No. is the number of results predicted by chance to have a
       score greater than or equal to the score of the result being printed,
       and is derived by analysis of the total score distribution.
```

```
                                    SUMMARIES
                    %
Result             Query
  No.    Score   Match  Length  DB  ID                      Description
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      1    548    65.5    117   1   HV1G_HUMAN              P23083 homo sapien
      2    533.5  63.7    498   2   Q6N041_HUMAN            Q6n041 homo sapien
      3    528.5  63.1    518   2   Q6N030_HUMAN            Q6n030 homo sapien
      4    520    62.1    480   2   Q6P089_HUMAN            Q6p089 homo sapien
```

5	511	61.1	519	2	Q5EBM2_HUMAN	Q5ebm2 homo sapien
6	509	60.8	497	2	Q8WY24_HUMAN	Q8wy24 homo sapien
7	503.5	60.2	500	2	Q9BRV0_HUMAN	Q9brv0 homo sapien
8	502	60.0	500	2	Q6N091_HUMAN	Q6n091 homo sapien
9	493.5	59.0	469	2	Q7Z7P5_HUMAN	Q7z7p5 homo sapien
10	493	58.9	150	2	Q9Y298_HUMAN	Q9y298 homo sapien
11	489.5	58.5	147	1	HV1C_HUMAN	P01744 homo sapien
12	489.5	58.5	159	2	Q96QS0_HUMAN	Q96qs0 homo sapien
13	486	58.1	117	1	HV1B_HUMAN	P01743 homo sapien
14	476	56.9	119	2	Q9UL94_HUMAN	Q9ul94 homo sapien
15	476	56.9	125	2	Q9UL95_HUMAN	Q9ul95 homo sapien
16	475	56.8	157	2	O95978_HUMAN	O95978 homo sapien
17	467	55.8	208	2	Q6ZP87_HUMAN	Q6zp87 homo sapien
18	466.5	55.7	496	2	Q96DK0_HUMAN	Q96dk0 homo sapien
19	464.5	55.5	139	1	HV07_MOUSE	P01751 mus musculu
20	459.5	54.9	124	2	Q9UL92_HUMAN	Q9ul92 homo sapien
21	459.5	54.9	475	2	Q6N095_HUMAN	Q6n095 homo sapien
22	458	54.7	473	2	Q9D8L4_MOUSE	Q9d8l4 mus musculu
23	456	54.5	138	1	HV48_MOUSE	P03980 mus musculu
24	450	53.8	616	2	Q504M7_MOUSE	Q504m7 mus musculu
25	448	53.5	458	2	Q5BJZ2_RAT	Q5bjz2 rattus norv
26	446	53.3	244	2	Q65ZC8_HUMAN	Q65zc8 homo sapien
27	445.5	53.2	598	2	Q568Y0_RAT	Q568y0 rattus norv
28	444.5	53.1	613	2	Q8VCX7_MOUSE	Q8vcx7 mus musculu
29	444	53.0	480	2	Q6PJF1_HUMAN	Q6pjf1 homo sapien
30	442	52.8	120	2	Q6NSA4_HUMAN	Q6nsa4 homo sapien
31	441.5	52.7	463	2	Q99LC4_MOUSE	Q99lc4 mus musculu
32	441.5	52.7	482	2	Q8K172_MOUSE	Q8k172 mus musculu
33	441	52.7	468	2	Q569W9_MOUSE	Q569w9 mus musculu
34	440	52.6	168	2	Q8VDC9_MOUSE	Q8vdc9 mus musculu
35	439.5	52.5	137	1	HV11_MOUSE	P01755 mus musculu
36	437	52.2	477	2	Q569B1_RAT	Q569b1 rattus norv
37	435.5	52.0	484	2	Q3SYJ4_MOUSE	Q3syj4 mus musculu
38	433	51.7	475	2	Q5FVP3_RAT	Q5fvp3 rattus norv
39	432.5	51.7	591	2	Q4QQW0_RAT	Q4qqw0 rattus norv
40	432	51.6	506	2	Q6MZW0_HUMAN	Q6mzw0 homo sapien
41	430.5	51.4	488	2	Q8K0F2_MOUSE	Q8k0f2 mus musculu
42	428	51.1	483	2	Q4VAB6_MOUSE	Q4vab6 mus musculu
43	427.5	51.1	465	2	Q6PJB2_MOUSE	Q6pjb2 mus musculu
44	425.5	50.8	480	2	Q2NLC3_MOUSE	Q2nlc3 mus musculu
45	425	50.8	470	2	Q7TMK1_MOUSE	Q7tmk1 mus musculu

ALIGNMENTS

RESULT 1
HV1G_HUMAN
ID   HV1G_HUMAN   STANDARD;   PRT;   117 AA.
AC   P23083;
DT   01-NOV-1991, integrated into UniProtKB/Swiss-Prot.
DT   01-NOV-1991, sequence version 1.
DT   07-MAR-2006, entry version 36.
DE   Ig heavy chain V-I region V35 precursor.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   NUCLEOTIDE SEQUENCE [GENOMIC DNA].

SCORE Search Results Details for Application 10044569 and Search Result us-10-044-569b-8.rag.

Score Home Page | Retrieve Application List | SCORE System Overview | SCORE FAQ | Comments / Suggestions

This page gives you Search Results detail for the Application 10044569 and Search Result us-10-044-569b-8.rag.

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OM protein - protein search, using sw model

Run on:         August  9, 2006, 01:42:08 ; Search time 105.738 Seconds
                                            (without alignments)
                                            618.341 Million cell updates/sec

Title:          US-10-044-569B-8
Perfect score:  738
Sequence:       1 METPAQLLFLLLLWLPDTTG..........TKVEIKRTVAAPSVFIFPPS 143

Scoring table:  BLOSUM62
                Gapop 10.0 , Gapext 0.5

Searched:       2589679 seqs, 457216429 residues

Total number of hits satisfying chosen parameters:      2589679

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :      A_Geneseq_8:*
                1:  geneseqp1980s:*
                2:  geneseqp1990s:*
                3:  geneseqp2000s:*
                4:  geneseqp2001s:*
                5:  geneseqp2002s:*
                6:  geneseqp2003as:*
                7:  geneseqp2003bs:*
                8:  geneseqp2004s:*
                9:  geneseqp2005s:*
                10:  geneseqp2006s:*

     Pred. No. is the number of results predicted by chance to have a
     score greater than or equal to the score of the result being printed,
     and is derived by analysis of the total score distribution.

                            SUMMARIES
```

```
               %
Result        Query
  No.  Score  Match Length  DB  ID                  Description
-------------------------------------------------------------------------------
     1   738  100.0    143   4  AAB47061            Aab47061 Light cha
     2   738  100.0    143   5  AAO18879            Aao18879 Human KRI
     3   730   98.9    143   9  ADY34084            Ady34084 Factor VI
     4 684.5   92.8    235   9  AEA41059            Aea41059 Anti-M-CS
     5 680.5   92.2    235   9  AEA41041            Aea41041 Anti-M-CS
     6 676.5   91.7    235   9  AEA41049            Aea41049 Anti-M-CS
     7   667   90.4    234   7  ADE28481            Ade28481 Human ant
     8 666.5   90.3    235   3  AAY93702            Aay93702 The kappa
     9 666.5   90.3    235   3  AAY93729            Aay93729 The kappa
    10 666.5   90.3    235   6  AAE35884            Aae35884 Human 4.1
    11 666.5   90.3    235   9  AED04279            Aed04279 Human ant
    12 666.5   90.3    235   9  AED04315            Aed04315 Human ant
    13   664   90.0    288   9  ADY34106            Ady34106 Factor VI
    14 662.5   89.8    236  10  AEF73710            Aef73710 Human IL-
    15   660   89.4    236   5  AAU74299            Aau74299 Anti-huma
    16   659   89.3    236   9  ADZ70600            Adz70600 Human pro
    17 658.5   89.2    235   6  ABP71366            Abp71366 Anti-OPGL
    18   655   88.8    236   9  ADZ57699            Adz57699 Anti-cMet
    19 654.5   88.7    142   4  AAB47060            Aab47060 Light cha
    20 654.5   88.7    142   5  AAO18877            Aao18877 Human B02
    21 654.5   88.7    233   3  AAY93704            Aay93704 The kappa
    22 654.5   88.7    233   3  AAY93731            Aay93731 The kappa
    23 654.5   88.7    233   6  AAE35886            Aae35886 Human 4.8
    24 654.5   88.7    233   9  AED04283            Aed04283 Human ant
    25 654.5   88.7    233   9  AED04319            Aed04319 Human ant
    26 653.5   88.6    235   9  AED14792            Aed14792 Ab D anti
    27   652   88.3    236   5  AAU74301            Aau74301 Anti-huma
    28 649.5   88.0    150   2  AAW40069            Aaw40069 Human mon
    29 649.5   88.0    150   4  AAE00946            Aae00946 Human mon
    30 649.5   88.0    150   8  ADO52287            Ado52287 Human ant
    31   645   87.4    234   3  AAY93733            Aay93733 The kappa
    32   645   87.4    234   3  AAY93708            Aay93708 The kappa
    33   645   87.4    234   6  AAE35888            Aae35888 Human 6.1
    34   645   87.4    234   9  AED04287            Aed04287 Human ant
    35   645   87.4    234   9  AED04327            Aed04327 Human ant
    36 641.5   86.9    150   7  ABU10485            Abu10485 Human C-a
    37 633.5   85.8    239   8  ADK70470            Adk70470 Respirato
    38 630.5   85.4    235  10  AEE86006            Aee86006 Anthrax t
    39 629.5   85.3    235   8  ADM41573            Adm41573 Anti-inte
    40   627   85.0    234   7  ADE28473            Ade28473 Human ant
    41   623   84.4    236   9  ADZ51040            Adz51040 Amino aci
    42   622   84.3    131   6  ABP57366            Abp57366 Anti-TRAI
    43 619.5   83.9    130   6  ADA43061            Ada43061 Human ant
    44 619.5   83.9    238   6  ABR41582            Abr41582 Human DIT
    45   614   83.2    127   9  ADW76948            Adw76948 RG1 C lig
```

ALIGNMENTS

RESULT 1
AAB47061
ID   AAB47061 standard; protein; 143 AA.
XX
AC   AAB47061;
XX
DT   08-MAY-2001 (first entry)

SCORE Search Results Details for Application 10044569 and Search Result us-10-044-569b-8.rai.

This page gives you Search Results detail for the Application 10044569 and Search Result us-10-044-569b-8.rai.

start

```
                        GenCore version 5.1.9
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OM protein - protein search, using sw model

Run on:          August  9, 2006, 01:59:49 ; Search time 27.8257 Seconds
                                             (without alignments)
                                             449.831 Million cell updates/sec

Title:          US-10-044-569B-8
Perfect score:  738
Sequence:       1 METPAQLLFLLLLWLPDTTG..........TKVEIKRTVAAPSVFIFPPS 143

Scoring table:  BLOSUM62
                Gapop 10.0 , Gapext 0.5

Searched:       650591 seqs, 87530628 residues

Total number of hits satisfying chosen parameters:       650591

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :      Issued_Patents_AA:*
                1:  /EMC_Celerra_SIDS3/ptodata/2/iaa/5_COMB.pep:*
                2:  /EMC_Celerra_SIDS3/ptodata/2/iaa/6_COMB.pep:*
                3:  /EMC_Celerra_SIDS3/ptodata/2/iaa/7_COMB.pep:*
                4:  /EMC_Celerra_SIDS3/ptodata/2/iaa/H_COMB.pep:*
                5:  /EMC_Celerra_SIDS3/ptodata/2/iaa/PCTUS_COMB.pep:*
                6:  /EMC_Celerra_SIDS3/ptodata/2/iaa/RE_COMB.pep:*
                7:  /EMC_Celerra_SIDS3/ptodata/2/iaa/backfiles1.pep:*

        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
        and is derived by analysis of the total score distribution.

                            SUMMARIES
                   %
Result          Query
  No.    Score  Match Length DB   ID                              Description
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  1   666.5   90.3    235   2   US-09-472-087-14        Sequence 14, Appl
  2   666.5   90.3    235   2   US-09-472-087-65        Sequence 65, Appl
  3     660   89.4    236   2   US-09-859-053-34        Sequence 34, Appl
  4   654.5   88.7    233   2   US-09-472-087-15        Sequence 15, Appl
  5   654.5   88.7    233   2   US-09-472-087-67        Sequence 67, Appl
  6     652   88.3    236   2   US-09-859-053-38        Sequence 38, Appl
  7   649.5   88.0    150   2   US-08-862-124-5         Sequence 5, Appli
  8     645   87.4    234   2   US-09-472-087-17        Sequence 17, Appl
  9     645   87.4    234   2   US-09-472-087-69        Sequence 69, Appl
 10     604   81.8    134   1   US-08-405-034-4         Sequence 4, Appli
 11     585   79.3    234   2   US-09-848-832-4         Sequence 4, Appli
 12   583.5   79.1    129   1   US-08-480-774A-4        Sequence 4, Appli
 13     575   77.9    226   2   US-09-456-090A-42       Sequence 42, Appl
 14     575   77.9    226   2   US-09-453-234-42        Sequence 42, Appl
 15     571   77.4    226   2   US-09-456-090A-50       Sequence 50, Appl
 16     571   77.4    226   2   US-09-456-090A-86       Sequence 86, Appl
 17     571   77.4    226   2   US-09-453-234-50        Sequence 50, Appl
 18     571   77.4    226   2   US-09-453-234-86        Sequence 86, Appl
 19     569   77.1    226   2   US-09-456-090A-80       Sequence 80, Appl
 20     569   77.1    226   2   US-09-453-234-80        Sequence 80, Appl
 21     567   76.8    224   2   US-09-456-090A-52       Sequence 52, Appl
 22     567   76.8    224   2   US-09-453-234-52        Sequence 52, Appl
 23     566   76.7    226   2   US-09-456-090A-72       Sequence 72, Appl
 24     566   76.7    226   2   US-09-453-234-72        Sequence 72, Appl
 25     564   76.4    116   1   US-08-053-131-183       Sequence 183, App
 26     564   76.4    116   1   US-08-096-762-183       Sequence 183, App
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 28     564   76.4    116   2   US-08-758-417A-311      Sequence 311, App
 29     564   76.4    226   2   US-09-456-090A-38       Sequence 38, Appl
 30     564   76.4    226   2   US-09-453-234-38        Sequence 38, Appl
 31     560   75.9    234   2   US-09-049-672A-6        Sequence 6, Appli
 32     559   75.7    226   2   US-09-456-090A-74       Sequence 74, Appl
 33     559   75.7    226   2   US-09-453-234-74        Sequence 74, Appl
 34     554   75.1    224   2   US-09-456-090A-76       Sequence 76, Appl
 35     554   75.1    224   2   US-09-453-234-76        Sequence 76, Appl
 36     553   74.9    224   2   US-09-456-090A-44       Sequence 44, Appl
 37     553   74.9    224   2   US-09-456-090A-78       Sequence 78, Appl
 38     553   74.9    224   2   US-09-453-234-44        Sequence 44, Appl
 39     553   74.9    224   2   US-09-453-234-78        Sequence 78, Appl
 40     552   74.8    238   2   US-09-499-662-107       Sequence 107, App
 41     549   74.4    224   2   US-09-456-090A-40       Sequence 40, Appl
 42     549   74.4    224   2   US-09-453-234-40        Sequence 40, Appl
 43     545   73.8    235   2   US-08-812-586-16        Sequence 16, Appl
 44     545   73.8    235   2   US-09-535-832A-17       Sequence 17, Appl
 45     540   73.2    238   2   US-09-499-662-50        Sequence 50, Appl
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ALIGNMENTS

RESULT 1
US-09-472-087-14
; Sequence 14, Application US/09472087
; Patent No. 6682736
; GENERAL INFORMATION:
; APPLICANT: HANSON, DOUGLAS C.
; APPLICANT: NEVEU, MARK J.
; APPLICANT: MUELLER, EILLEN E.
; APPLICANT: HANKE, JEFFREY H.
; APPLICANT: GILMAN, STEVEN C.

SCORE Search Results Details for Application 10044569 and Search Result us-10-044-569b-8.rapbm.

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OM protein - protein search, using sw model

Run on:          August  9, 2006, 02:25:55 ; Search time 91.22 Seconds
                                             (without alignments)
                                             726.154 Million cell updates/sec

Title:           US-10-044-569B-8
Perfect score:   738
Sequence:        1 METPAQLLFLLLLWLPDTTG..........TKVEIKRTVAAPSVFIFPPS 143

Scoring table:   BLOSUM62
                 Gapop 10.0 , Gapext 0.5

Searched:        2097797 seqs, 463214858 residues

Total number of hits satisfying chosen parameters:      2097797

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
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                 Listing first 45 summaries

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      Pred. No. is the number of results predicted by chance to have a
      score greater than or equal to the score of the result being printed,
      and is derived by analysis of the total score distribution.

                              SUMMARIES
                     %
Result           Query
   No.   Score  Match Length DB  ID                          Description
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1	738	100.0	143	4	US-10-044-569B-8	Sequence 8, Appli
2	684.5	92.8	235	5	US-10-938-353-60	Sequence 60, Appl
3	680.5	92.2	235	5	US-10-938-353-32	Sequence 32, Appl
4	676.5	91.7	235	5	US-10-938-353-44	Sequence 44, Appl
5	667	90.4	234	4	US-10-292-088-88	Sequence 88, Appl
6	666.5	90.3	235	4	US-10-153-382-7	Sequence 7, Appli
7	666.5	90.3	235	5	US-10-612-497-14	Sequence 14, Appl
8	666.5	90.3	235	5	US-10-612-497-65	Sequence 65, Appl
9	666.5	90.3	235	5	US-10-776-649-14	Sequence 14, Appl
10	666.5	90.3	235	5	US-10-776-649-65	Sequence 65, Appl
11	666.5	90.3	235	6	US-11-085-368-7	Sequence 7, Appli
12	666.5	90.3	235	6	US-11-085-368-43	Sequence 43, Appl
13	666.5	90.3	235	6	US-11-128-900-14	Sequence 14, Appl
14	666.5	90.3	235	6	US-11-128-900-65	Sequence 65, Appl
15	660	89.4	236	3	US-09-859-053-34	Sequence 34, Appl
16	660	89.4	236	4	US-10-800-250-34	Sequence 34, Appl
17	660	89.4	236	4	US-10-625-105-34	Sequence 34, Appl
18	658.5	89.2	235	4	US-10-180-648-4	Sequence 4, Appli
19	655	88.8	236	5	US-10-910-901-8	Sequence 8, Appli
20	654.5	88.7	142	4	US-10-044-569B-4	Sequence 4, Appli
21	654.5	88.7	233	4	US-10-153-382-11	Sequence 11, Appl
22	654.5	88.7	233	5	US-10-612-497-15	Sequence 15, Appl
23	654.5	88.7	233	5	US-10-612-497-67	Sequence 67, Appl
24	654.5	88.7	233	5	US-10-776-649-15	Sequence 15, Appl
25	654.5	88.7	233	5	US-10-776-649-67	Sequence 67, Appl
26	654.5	88.7	233	6	US-11-085-368-11	Sequence 11, Appl
27	654.5	88.7	233	6	US-11-085-368-47	Sequence 47, Appl
28	654.5	88.7	233	6	US-11-128-900-15	Sequence 15, Appl
29	654.5	88.7	233	6	US-11-128-900-67	Sequence 67, Appl
30	653.5	88.6	235	6	US-11-086-289-16	Sequence 16, Appl
31	652	88.3	236	3	US-09-859-053-38	Sequence 38, Appl
32	652	88.3	236	4	US-10-800-250-38	Sequence 38, Appl
33	652	88.3	236	4	US-10-625-105-38	Sequence 38, Appl
34	649.5	88.0	150	3	US-09-782-397-5	Sequence 5, Appli
35	649.5	88.0	150	4	US-10-651-453-5	Sequence 5, Appli
36	645	87.4	234	4	US-10-153-382-15	Sequence 15, Appl
37	645	87.4	234	5	US-10-612-497-17	Sequence 17, Appl
38	645	87.4	234	5	US-10-612-497-69	Sequence 69, Appl
39	645	87.4	234	5	US-10-776-649-17	Sequence 17, Appl
40	645	87.4	234	5	US-10-776-649-69	Sequence 69, Appl
41	645	87.4	234	6	US-11-085-368-15	Sequence 15, Appl
42	645	87.4	234	6	US-11-085-368-55	Sequence 55, Appl
43	645	87.4	234	6	US-11-128-900-17	Sequence 17, Appl
44	645	87.4	234	6	US-11-128-900-69	Sequence 69, Appl
45	629.5	85.3	235	4	US-10-656-769-38	Sequence 38, Appl

ALIGNMENTS

RESULT 1
US-10-044-569B-8
; Sequence 8, Application US/10044569B
; Publication No. US20030175268A1
; GENERAL INFORMATION:
; APPLICANT: D. Collen Research Foundation vzw
; APPLICANT: Jacquemin, Marc G
; APPLICANT: Saint-Remy, Jean-Marie R
; TITLE OF INVENTION: Method and pharmaceutical composition for preventing
; TITLE OF INVENTION: and/or treating systemic inflammatory response syndrome
; FILE REFERENCE: C1968

SCORE Search Results Details for Application 10044569 and Search Result us-10-044-569b-8.rapbn.

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OM protein - protein search, using sw model

Run on:          August  9, 2006, 02:27:00 ; Search time 14.0338 Seconds
                                             (without alignments)
                                             681.831 Million cell updates/sec

Title:           US-10-044-569B-8
Perfect score:   738
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Searched:        236815 seqs, 66914042 residues

Total number of hits satisfying chosen parameters:      236815

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

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           3:    /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US07_NEW_PUB.pep:*
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           8:    /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US60_NEW_PUB.pep:*

    Pred. No. is the number of results predicted by chance to have a
    score greater than or equal to the score of the result being printed,
    and is derived by analysis of the total score distribution.

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                     %
Result               Query
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2	684.5	92.8	235	7	US-11-375-221-60	Sequence 60, Appl
3	680.5	92.2	235	7	US-11-375-221-32	Sequence 32, Appl
4	676.5	91.7	235	7	US-11-375-221-44	Sequence 44, Appl
5	667	90.4	234	7	US-11-211-917-88	Sequence 88, Appl
6	664	90.0	288	7	US-11-298-560-26	Sequence 26, Appl
7	654.5	88.7	142	7	US-11-298-560-48	Sequence 48, Appl
8	627	85.0	234	7	US-11-211-917-72	Sequence 72, Appl
9	571	77.4	234	7	US-11-375-221-12	Sequence 12, Appl
10	523.5	70.9	223	7	US-11-365-556-305	Sequence 305, App
11	513.5	69.6	109	7	US-11-375-221-114	Sequence 114, App
12	500	67.8	214	6	US-10-515-429-75	Sequence 75, Appl
13	495.5	67.1	130	7	US-11-293-697-4264	Sequence 4264, Ap
14	494	66.9	234	7	US-11-211-917-24	Sequence 24, Appl
15	493.5	66.9	108	7	US-11-211-917-113	Sequence 113, App
16	491	66.5	107	7	US-11-211-917-84	Sequence 84, Appl
17	491	66.5	234	6	US-10-511-436A-92	Sequence 92, Appl
18	490	66.4	214	6	US-10-515-429-72	Sequence 72, Appl
19	487	66.0	234	7	US-11-211-917-48	Sequence 48, Appl
20	486	65.9	222	7	US-11-365-556-307	Sequence 307, App
21	484	65.6	236	7	US-11-375-221-20	Sequence 20, Appl
22	482.5	65.4	110	7	US-11-254-679-34	Sequence 34, Appl
23	481	65.2	236	7	US-11-375-221-52	Sequence 52, Appl
24	479.5	65.0	109	6	US-10-994-679-70	Sequence 70, Appl
25	479	64.9	234	7	US-11-375-221-4	Sequence 4, Appli
26	478	64.8	234	6	US-10-546-594-132	Sequence 132, App
27	478	64.8	234	7	US-11-375-221-8	Sequence 8, Appli
28	478	64.8	236	7	US-11-375-221-36	Sequence 36, Appl
29	474	64.2	236	7	US-11-375-221-16	Sequence 16, Appl
30	473.5	64.2	110	7	US-11-304-986-16	Sequence 16, Appl
31	473	64.1	238	7	US-11-298-020-10	Sequence 10, Appl
32	471	63.8	236	7	US-11-375-221-56	Sequence 56, Appl
33	468	63.4	236	7	US-11-375-221-48	Sequence 48, Appl
34	467.5	63.3	108	6	US-10-821-930-21	Sequence 21, Appl
35	467	63.3	214	7	US-11-254-182-40	Sequence 40, Appl
36	466	63.1	128	7	US-11-290-687-8	Sequence 8, Appli
37	466	63.1	171	6	US-10-981-300-10	Sequence 10, Appl
38	466	63.1	236	7	US-11-375-221-28	Sequence 28, Appl
39	464.5	62.9	109	6	US-10-994-679-62	Sequence 62, Appl
40	464	62.9	240	7	US-11-375-221-24	Sequence 24, Appl
41	463	62.7	236	7	US-11-290-687-25	Sequence 25, Appl
42	461	62.5	236	7	US-11-290-687-27	Sequence 27, Appl
43	460	62.3	107	7	US-11-211-917-100	Sequence 100, App
44	459	62.2	96	7	US-11-221-902-67	Sequence 67, Appl
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ALIGNMENTS

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; Sequence 4, Application US/11298560
; Publication No. US20060115474A1
; GENERAL INFORMATION:
;   APPLICANT: Jacquemin, Marc
;   APPLICANT: Saint-Remy, Jean-Marie
;   TITLE OF INVENTION: Ligands For Use In Therapeutic Compositions For The Treatment o
;   TITLE OF INVENTION: Hemostasis Disorders

SCORE Seal

This page gives you Search Results detail for the Application 10044569 and Search Result us-10-0∢
start

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OM protein - protein search, using sw model

Run on:          August  9, 2006, 01:50:34 ; Search time 17.1794 Seconds
                                             (without alignments)
                                             800.903 Million cell updates/sec

Title:           US-10-044-569B-8
Perfect score:   738
Sequence:        1 METPAQLLFLLLLWLPDTTG..........TKVEIKRTVAAPSVFIFPPS 143

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                 Gapop 10.0 , Gapext 0.5

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Total number of hits satisfying chosen parameters:      283416

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Post-processing: Minimum Match 0%
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                 Listing first 45 summaries

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         Pred. No. is the number of results predicted by chance to have a
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         and is derived by analysis of the total score distribution.

                              SUMMARIES
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3	608.5	82.5	129	1	K3HUHA	Ig kappa chain pre
4	598.5	81.1	129	1	K3HUHI	Ig kappa chain pre
5	596.5	80.8	129	2	S49532	anti-Sm antibody V
6	590.5	80.0	128	2	S20636	Ig kappa chain V r
7	585.5	79.3	129	2	S46369	IG light chain var
8	585.5	79.3	134	2	S38643	Ig kappa chain V r

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 9     576    78.0   129   2   S40325          Ig kappa chain - h
10     572.5  77.6   129   2   A32274          Ig kappa chain pre
11     570.5  77.3   130   2   S20637          Ig kappa chain V r
12     569    77.1   131   2   S40346          Ig kappa chain V-J
13     566.5  76.8   130   2   S40360          Ig kappa chain - h
14     564    76.4   116   2   B27594          Ig kappa chain pre
15     563.5  76.4   121   2   S40327          Ig kappa chain - h
16     552.5  74.9   116   2   C27594          Ig kappa chain pre
17     548.5  74.3   124   2   S20633          Ig kappa chain - h
18     537    72.8   116   2   B25521          Ig kappa chain pre
19     535    72.5   128   1   K3HU41          Ig kappa chain pre
20     533.5  72.3   127   2   S40380          Ig kappa chain V-J
21     533.5  72.3   129   2   S40363          Ig kappa chain - h
22     532.5  72.2   215   2   A23746          Ig kappa chain V-I
23     531    72.0   129   2   S29627          Ig kappa chain V r
24     527    71.4   128   2   S40379          Ig kappa chain V-J
25     526    71.3   114   2   S46375          Ig kappa chain V-J
26     525    71.1   125   2   S40344          Ig kappa chain V-J
27     525    71.1   128   2   S40345          Ig kappa chain V-J
28     524    71.0   128   2   A56701          Ig kappa chain V r
29     519.5  70.4   215   2   JE0242          Ig kappa chain NIG
30     518    70.2   128   2   S40343          Ig kappa chain V-J
31     510.5  69.2   109   2   A30608          Ig kappa chain V-I
32     510.5  69.2   131   2   S40328          Ig kappa chain - h
33     506.5  68.6   115   1   K3HUVG          Ig kappa chain pre
34     506.5  68.6   215   2   JE0244          Ig kappa chain NIG
35     505.5  68.5   109   2   B30601          Ig kappa chain V-I
36     503    68.2   116   1   K3HUVH          Ig kappa chain pre
37     503    68.2   116   2   S41817          Ig kappa chain V r
38     502.5  68.1   109   2   C30601          Ig kappa chain V-I
39     501.5  68.0   109   2   G30607          Ig kappa chain V-I
40     501    67.9   110   2   E30607          Ig kappa chain V-I
41     501    67.9   111   2   S40359          Ig kappa chain V-J
42     499.5  67.7   109   2   D30601          Ig kappa chain V-I
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44     497.5  67.4   109   2   H30601          Ig kappa chain V-I
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                              ALIGNMENTS


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C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 21-Jan-2000
C;Accession: S20631
R;Lee, S.K.; Bridges, L.S.; Koopman, W.J.; Schroeder, H.W.
submitted to the EMBL Data Library, April 1992
A;Reference number: S20631
A;Accession: S20631
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-145
A;Cross-references: UNIPARC:UPI00001163DD; EMBL:Z11903; NID:g33156; PIDN:CAA77955.1; P
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;36-111/Domain: immunoglobulin homology

    Query Match             84.8%;  Score 625.5;  DB 2;  Length 145;
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SCORE Search Results Details for Application 10044569 and Search Result us-10-044-569b-8.rup.

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start

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OM protein - protein search, using sw model

Run on:        August  9, 2006, 01:43:08 ; Search time 133.563 Seconds
                                          (without alignments)
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Title:         US-10-044-569B-8
Perfect score: 738
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Scoring table: BLOSUM62
               Gapop 10.0 , Gapext 0.5

Searched:      2849598 seqs, 925015592 residues

Total number of hits satisfying chosen parameters:      2849598

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
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Database :      UniProt_7.2:*
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               2:  uniprot_trembl:*

     Pred. No. is the number of results predicted by chance to have a
     score greater than or equal to the score of the result being printed,
     and is derived by analysis of the total score distribution.
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SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
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3	642.5	87.1	235	2	Q6GMV9_HUMAN	Q6gmv9 homo sapien
4	639.5	86.7	235	2	Q6PJF2_HUMAN	Q6pjf2 homo sapien

5	608.5	82.5	129	1	KV3L_HUMAN	P18135 homo sapien
6	598.5	81.1	129	1	KV3M_HUMAN	P18136 homo sapien
7	586.5	79.5	235	2	Q6GMW0_HUMAN	Q6gmw0 homo sapien
8	575	77.9	234	2	Q569I9_HUMAN	Q569i9 homo sapien
9	535	72.5	128	1	KV3K_HUMAN	P06311 homo sapien
10	531.5	72.0	129	1	KV3H_HUMAN	P04207 homo sapien .
11	506.5	68.6	115	1	KV3I_HUMAN	P04433 homo sapien
12	505.5	68.5	109	2	Q9UL78_HUMAN	Q9ul78 homo sapien
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15	489.5	66.3	109	1	KV3B_HUMAN	P01620 homo sapien
16	489.5	66.3	109	1	KV3E_HUMAN	P01623 homo sapien
17	486	65.9	236	2	Q6GMX8_HUMAN	Q6gmx8 homo sapien
18	483.5	65.5	109	2	Q9UL86_HUMAN	Q9ul86 homo sapien
19	481.5	65.2	109	1	KV3D_HUMAN	P01622 homo sapien
20	479	64.9	234	2	Q7Z473_HUMAN	Q7z473 homo sapien
21	473	64.1	236	2	Q6PIH4_HUMAN	Q6pih4 homo sapien
22	473	64.1	236	2	Q6PIT5_HUMAN	Q6pit5 homo sapien
23	471	63.8	236	2	Q6GMX0_HUMAN	Q6gmx0 homo sapien
24	470	63.7	236	2	Q6GMW1_HUMAN	Q6gmw1 homo sapien
25	468	63.4	236	2	Q6GMX9_HUMAN	Q6gmx9 homo sapien
26	464.5	62.9	109	1	KV3G_HUMAN	P04206 homo sapien
27	461	62.5	236	2	Q502W4_HUMAN	Q502w4 homo sapien
28	460.5	62.4	239	2	Q8NEK0_HUMAN	Q8nek0 homo sapien
29	459	62.2	240	2	Q6PIH6_HUMAN	Q6pih6 homo sapien
30	457.5	62.0	108	1	KV3A_HUMAN	P01619 homo sapien
31	457	61.9	234	2	Q5EFE6_HUMAN	Q5efe6 homo sapien
32	456	61.8	100	1	KV3C_HUMAN	P01621 homo sapien
33	456	61.8	189	2	Q569I7_HUMAN	Q569i7 homo sapien
34	455	61.7	236	2	Q7Z3Y4_HUMAN	Q7z3y4 homo sapien
35	446	60.4	240	2	Q52L64_MOUSE	Q52l64 mus musculu
36	443.5	60.1	239	2	Q8TCD0_HUMAN	Q8tcd0 homo sapien
37	437	59.2	238	2	Q66JS7_MOUSE	Q66js7 mus musculu
38	436.5	59.1	109	2	Q9UL85_HUMAN	Q9ul85 homo sapien
39	422.5	57.2	109	1	KV3F_HUMAN	P01624 homo sapien
40	421	57.0	238	2	Q58EU4_MOUSE	Q58eu4 mus musculu
41	419.5	56.8	239	2	Q6P491_HUMAN	Q6p491 homo sapien
42	418	56.6	237	2	Q7SZ36_XENLA	Q7sz36 xenopus lae
43	417.5	56.6	133	1	KV4B_HUMAN	P06313 homo sapien
44	411	55.7	108	2	Q9UL83_HUMAN	Q9ul83 homo sapien
45	409.5	55.5	239	2	Q58EU8_MOUSE	Q58eu8 mus musculu

ALIGNMENTS

RESULT 1
Q6P5S8_HUMAN
ID   Q6P5S8_HUMAN   PRELIMINARY;   PRT;   236 AA.
AC   Q6P5S8;
DT   05-JUL-2004, integrated into UniProtKB/TrEMBL.
DT   05-JUL-2004, sequence version 1.
DT   07-FEB-2006, entry version 15.
DE   Hypothetical protein.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.